

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 25, 2003, 14:38:41 ; Search time 26.8605 Seconds
(Without alignments)
843.812 Million cell updates/sec

Title: US-09-622-613B-19
Perfect score: 599
Sequence: 1 OMNATFOOKHIKTPICNT.....ICVKCENQYFVHAGIGRCP 110

Scoring table: BIOSUM52
Gapop 10.0, Gapext 0.5

Searched: 671580/seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP archaea: *
2: SP bacteria: *
3: SP fungi: *
4: SP human: *
5: SP invertebrate: *
6: SP mammal: *
7: SP mhc: *
8: SP organelle: *
9: SP phage: *
10: SP plant: *
11: SP rodent: *
12: SP virus: *
13: SP vertebrate: *
14: SP unclassified: *
15: SP viirus: *
16: SP bacteriap: *
17: SP archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|---------|---------------------|
| 1 | 579.5 | 96.7 | 133 | 09PWR7 | 09PWR7 rana catesb |
| 2 | 548.5 | 91.6 | 133 | 098SM0 | 098SM0 rana catesb |
| 3 | 482.5 | 80.6 | 133 | 098SM2 | 098SM2 rana catesb |
| 4 | 468.5 | 78.2 | 133 | 098SL9 | 098SL9 rana catesb |
| 5 | 461.5 | 77.0 | 133 | 098SL8 | 098SL8 rana catesb |
| 6 | 443.5 | 74.0 | 133 | 098SM1 | 098SM1 rana catesb |
| 7 | 371 | 61.9 | 133 | 098P78 | 098P78 rana catesb |
| 8 | 271.5 | 45.3 | 127 | 0918V8 | 0918V8 rana catesb |
| 9 | 267.5 | 44.7 | 127 | 080UVX5 | 080UVX5 rana pipien |
| 10 | 241 | 40.2 | 129 | 09DPY6 | 09DPY6 rana catesb |
| 11 | 223.5 | 37.3 | 128 | 09DPY8 | 09DPY8 rana catesb |
| 12 | 221.5 | 37.0 | 128 | 09DPY7 | 09DPY7 rana catesb |
| 13 | 212.5 | 35.5 | 128 | 09DPY5 | 09DPY5 rana catesb |
| 14 | 166 | 27.7 | 169 | 09W738 | 09W738 xenopus lae |
| 15 | 122 | 20.4 | 170 | 09BEC1 | 09BEC1 tragulus ja |
| 16 | 120.5 | 20.1 | 163 | 09BDC2 | 09BDC2 antilocapra |

| | | | | | | |
|----|-------|------|-----|----|--------|--------------------|
| 17 | 120 | 20.0 | 150 | 11 | 08VD94 | 08VD94 beryllus bo |
| 18 | 118 | 19.7 | 150 | 11 | 08VD88 | 08VD88 ractus norv |
| 19 | 117.5 | 19.6 | 144 | 6 | 09BH14 | 09BH14 antilocapra |
| 20 | 115.5 | 19.3 | 116 | 6 | 09TWC0 | 09TWC0 sus scrofa |
| 21 | 115 | 18.9 | 150 | 11 | 08VD92 | 08VD92 ractus exul |
| 22 | 113.5 | 18.9 | 152 | 11 | 08VD89 | 08VD89 ractus norv |
| 23 | 112.5 | 18.8 | 119 | 6 | 09TV33 | 09TV33 bos taurus |
| 24 | 109.5 | 18.3 | 124 | 6 | 095NE6 | 095NE6 bubalus bub |
| 25 | 109 | 18.2 | 124 | 6 | 09BEC2 | 09BEC2 tragulus ja |
| 26 | 108.5 | 18.1 | 149 | 11 | 08VD95 | 08VD95 beryllus bo |
| 27 | 108 | 18.0 | 134 | 6 | 09BDB9 | 09BDB9 tragulus ja |
| 28 | 107.5 | 17.9 | 119 | 6 | 09TV30 | 09TV30 sagunus oe |
| 29 | 107.5 | 17.9 | 119 | 6 | 09TV28 | 09TV28 eulimur ful |
| 30 | 107.5 | 17.9 | 152 | 11 | 08VD84 | 08VD84 ractus tiom |
| 31 | 107.5 | 17.9 | 156 | 6 | 08S005 | 08S005 lagothrix l |
| 32 | 105.5 | 17.6 | 124 | 6 | 09TSP2 | 09TSP2 bos taurus |
| 33 | 105.5 | 17.6 | 156 | 6 | 08S006 | 08S006 ateles geof |
| 34 | 104.5 | 17.4 | 142 | 6 | 09BEC3 | 09BEC3 tragulus ja |
| 35 | 104.5 | 17.4 | 152 | 11 | 08VD90 | 08VD90 ractus fusc |
| 36 | 104.5 | 17.4 | 156 | 6 | 08S008 | 08S008 salmuri scl |
| 37 | 104.5 | 17.4 | 156 | 6 | 08S007 | 08S007 sagunus oe |
| 38 | 102.5 | 17.1 | 119 | 6 | 09TSP6 | 09TSP6 cercopithec |
| 39 | 102.5 | 17.1 | 149 | 11 | 08VD93 | 08VD93 ractus exul |
| 40 | 101.5 | 16.9 | 119 | 6 | 09TV32 | 09TV32 gorilla gor |
| 41 | 100.5 | 16.8 | 158 | 6 | 08SPV3 | 08SPV3 sagunus ja |
| 42 | 100 | 16.7 | 158 | 6 | 08SPV2 | 08SPV2 callithrix |
| 43 | 99.5 | 16.6 | 119 | 6 | 09TV31 | 09TV31 salmuri scl |
| 44 | 98.5 | 16.4 | 147 | 11 | 08VD87 | 08VD87 ractus ratl |
| 45 | 98.5 | 16.4 | 156 | 6 | 08SPV4 | 08SPV4 pygachrix n |

ALIGNMENTS

RESULT 1

| ID | Q9PWR7 | PRELIMINARY: | PRT: | 133 AA. |
|----|--|---------------------------------|--------------------|--|
| AC | Q9PWR7 | 01-MAY-2000 (TREMUR13, Created) | | |
| DT | 01-MAY-2000 (TREMUR13, Last sequence update) | | | |
| DT | 01-DEC-2001 (TREMUR13, Last annotation update) | | | |
| DE | Ribonuclease precursor. | | | |
| GN | RCR. | | | |
| OS | Rana catesbeiana (Bull frog). | | | |
| OC | Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: | | | |
| OC | Amphibia: Batrachia: Anura: Neobatrachia: Ranoidae: Rana: | | | |
| OX | NCBI_TaxID=8400; | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RP | TISSUE=LIVER: | | | |
| RC | MEDLINE=98165825; PubMed=9497370; | | | |
| RX | Huang H.C., Wang S.C., Liu Y.J., Lu S.C., Liao Y.D., | | | |
| RT | "The Rana catesbeiana rcr gene encoding a cytoxic ribonuclease. | | | |
| RT | Tissue distribution, cloning, purification, cytotoxicity, and active | | | |
| RT | residues for RNase activity." | | | |
| RL | J. Biol. Chem. 273:6395-6401(1998). | | | |
| DR | EMBL: AF039104; AD10702.1; | | | |
| DR | HSP: P11916; IBC4. | | | |
| DR | InterPro: IPR001427; RNaseA. | | | |
| DR | Pfam: PF00074; RNaseA; 1. | | | |
| DR | PRODOM: PD000535; RNaseA; 1. | | | |
| DR | SMART: SM00092; RNase_Pc; 1. | | | |
| DR | PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1. | | | |
| KW | Signal. | | | |
| FT | SIGNAL | 1 | 22 | POTENTIAL. |
| FT | CHAIN | 23 | 133 | RIBONUCLEASE. |
| SO | SEQUENCE | 133 AA; | 14762 MW; | A7D62594F7D16FOC CRC64; |
| QY | Query Match | 96.7%; | Score 579.5; | DB 13; |
| | Best Local Similarity | 96.4%; | Pred. NO. 2.8e-59; | Length 133; |
| | Matches 107; | Conservative 2; | Mismatches 1; | Indels 1; |
| | | | | Gaps 1; |
| | | | | 1 OMNATFOOKHIKTPICNT.....ICVKCENQYFVHAGIGRCP 110 |

Db 23 QNMATFOQKHIIPTIICNTIMDNIIYVGGCKRVNFTIISATTVKAICTGVINLV 82
 Oy 60 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 110
 Db 83 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 133

RESULT 2

098SMO

ID 098SMO PRELIMINARY; PRT; 133 AA.

AC 098SMO; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc208 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-21539506; PubMed-11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

bullfrog, Rana catesbeiana.";

RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351209; AAK30255.1;
 DR HSSP: P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 22 POTENTIAL.
 SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match
 Best Local Similarity 91.6%; Score 548.5; DB 13; Length 133;
 Matches 102; Conservative 2; Mismatches 6; Indels 1; Gaps 1;

Oy 1 QNMATFOQKHIIKPII-CNTILDNNIYVGGCKRVNFTIISATTVKAICTGVINLV 59
 Db 23 QNMATFOQKHIIKPII-CNTILDNNIYVGGCKRVNFTIISATTVKAICTGVINLV 82
 Oy 60 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 110
 Db 83 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 133

RESULT 3

098SM2

ID 098SM2 PRELIMINARY; PRT; 132 AA.

AC 098SM2; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-21539506; PubMed-11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 RN [2]
RP SEQUENCE FROM N.A.
 RP TISSUE=LIVER;

RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF351207; AAK30253.1;
 DR EMBL: AF359578; AAL87036.1;
 DR HSSP: P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 22 POTENTIAL.
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match
 Best Local Similarity 80.6%; Score 482.5; DB 13; Length 133;
 Matches 91; Conservative 5; Mismatches 13; Indels 1; Gaps 1;

Oy 1 QNMATFOQKHIIKPII-CNTILDNNIYVGGCKRVNFTIISATTVKAICTGVINLV 59
 Db 23 QNMATFOQKHIIKPII-CNTILDNNIYVGGCKRVNFTIISATTVKAICTGVINLV 82
 Oy 60 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 109
 Db 83 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 132

RESULT 4

098SL9

ID 098SL9 PRELIMINARY; PRT; 133 AA.

AC 098SL9; 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RNase A-type ribonuclease rc212 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-21539506; PubMed-11683320;

RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;

RT "Rapid diversification of RNase A superfamily ribonuclease from the

bullfrog, Rana catesbeiana.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351210; AAK30256.1;
 DR HSSP: P11916; IBC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL. 1 22 POTENTIAL.
 SQ SEQUENCE 133 AA; 14615 MW; C8785B236B2E54E CRC64;

Query Match
 Best Local Similarity 78.2%; Score 468.5; DB 13; Length 133;
 Matches 85; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

Oy 1 QNMATFOQKHIIKPII-CNTILDNNIYVGGCKRVNFTIISATTVKAICTGVINLV 59
 Db 23 QNMATFOQKHIIKPII-CNTILDNNIYVGGCKRVNFTIISATTVKAICTGVINLV 82
 Oy 60 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 110
 Db 83 LSTTRFOLNCTRTSTTPRCPPYSSRTETNYICVCKENQYPVHFAGIGRCP 133

RESULT 5

098SL8

ID 098SL8 PRELIMINARY; PRT: 133 AA.
AC 098SL8;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rnase A-type ribonuclease rc218 precursor.
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAC30257.1; -
DR HSSP; P11916; 1BC4
DR InterPro: IPR001427; RnaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR Prodom: PD000535; RnaseA; 1.
DR SMART; SM00092; RnaseA_Pc; 1.
DR PROSITE; PS00127; Rnase_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL
SO SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
POTENTIAL.

Query Match 77.0%; Score 461.5; DB 13; Length 133;
Best Local Similarity 74.8%; Pred. No. 1.2e-45;
Matches 83; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

OY 1 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 59
DB 23 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 82
OY 60 LSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 110
DB 83 LSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 133

RESULT 6
ID 098SM1 PRELIMINARY; PRT: 132 AA.
AC 098SM1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Rnase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351206; AAC30254.1; -
DR HSSP; P11916; 1BC4
DR InterPro: IPR001427; RnaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR Prodom: PD000535; RnaseA; 1.
DR SMART; SM00092; RnaseA_Pc; 1.
DR PROSITE; PS00127; Rnase_PANCREATIC; UNKNOWN_1.
KW Signal.
FT SIGNAL
SO SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
POTENTIAL.

Query Match 74.0%; Score 443.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 1.4e-43;

Matches 85; Conservative 7; Mismatches 17; Indels 1; Gaps 1;
OY 1 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 59
DB 23 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 82
OY 60 LSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 109
DB 83 LSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 132

RESULT 7
ID 09DF78 PRELIMINARY; PRT: 132 AA.
AC 09DF78;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RC-Rnasel ribonuclease precursor.
OS Rana catesbeiana (bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=LIVER;
RC TISSUE=LIVER;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]

OY 1 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 58
DB 22 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 81
OY 59 VLSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 109
DB 82 VLSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 132

Query Match 61.9%; Score 371; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 3.4e-35;
Matches 72; Conservative 9; Mismatches 28; Indels 2; Gaps 2;
OY 1 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 58
DB 22 ONMATPOOKHIIKPII-CNTILNNIYIVGGCKRVNFTFISSATVKAICGVINLVN 81
OY 59 VLSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 109
DB 82 VLSTTRFOLNCTRTSTPRPCPYSSRTETNYICVCKENQYVHPAGIGRC 132

RESULT 8
ID 0918V8 PRELIMINARY; PRT: 127 AA.
AC 0918V8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Onconase variant rap1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8404;

[1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=LIVER;
 RC MEDLINE=20330357; PubMed-10871370;
 RA Chen S.-L., Le S.-Y., Newton D.L., Mizel J.V. Jr., Rybak S.M.;
 RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
 3' UTR of unusual length and structure";
 RL Nucleic Acids Res. 28:2375-2382(2000).
 DR EMBL: AF165133; AAF76935.1;
 DR HSSP: P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea.1.
 DR ProDom: PD000535; RNasea.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 127 AA: 14491 MW: 8511DC5407AB69B CRC64:

Query Match 45.3%; Score 271.5; DB 13; Length 127;
 Best Local Similarity 47.7%; Pred. No. 1e-23;
 Matches 53; Conservative 16; Mismatches 33; Indels 9; Gaps 4;

OY 1 QNMATFOCKHIKT-PIICNTILDNNTIYVGQCKRVNFTIISATYKACTGYI-NLN 58
 DB 24 QDWLTFCKHLLTRDVCNIMSTNLF---HCKDKNTFYISREPEYKALCKGIASKN 79
 OY 59 VLSSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENCPVHPFAGIGRC 109
 DB 80 VLTISEFYLSDC---NVTISRCCKYKLRKSTNFCVTCENQAPVHFGVGIC 127

RESULT 9

O8UVX5 PRELIMINARY: PRT: 127 AA.

ID O8UVX5:
 AC O8UVX5:
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Oncoenase precursor.
 GN RPR.

OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCB1_TaxID=8404;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Liao Y.-D., Wang S.-C.;
 RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AF332139; AAL54383.1;
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea.1.
 DR ProDom: PD000535; RNasea.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 SQ SEQUENCE 127 AA: 14469 MW: 953F90D351CEEF3 CRC64:

Query Match 44.7%; Score 267.5; DB 13; Length 127;
 Best Local Similarity 47.7%; Pred. No. 3e-23;
 Matches 53; Conservative 16; Mismatches 33; Indels 9; Gaps 4;

OY 1 QNMATFOCKHIKT-PIICNTILDNNTIYVGQCKRVNFTIISATYKACTGYI-NLN 58
 DB 24 QDWLTFCKHLLTRDVCNIMSTNLF---HCKDKNTFYISREPEYKALCKGIASKN 79
 OY 59 VLSSTRFOLNCTRTSITPRCPYSSRTETNYICVCKENCPVHPFAGIGRC 109
 DB 80 VLTISEFYLSDC---NVTISRCCKYKLRKSTNFCVTCENQAPVHFGVGIC 127

RESULT 10
 O9DFY6 PRELIMINARY: PRT: 129 AA.

ID O9DFY6:
 AC O9DFY6:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase4 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCB1_TaxID=8400;
 RN 11
 RP SEQUENCE FROM N.A.
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN 12

SEQUENCE FROM N.A.

RC TISSUE=LIVER;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF242555; AAC31441.2;
 DR HSSP: P22069; 10NC.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnaasea.1.
 DR ProDom: PD000535; RNasea.1.
 DR SMART: SM00092; RNase_Pc.1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; UNKNOWN_1.
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 23 POTENTIAL.
 SQ SEQUENCE 129 AA: 14724 MW: 826A6282B10ABDA CRC64:

Query Match 40.2%; Score 241; DB 13; Length 129;
 Best Local Similarity 42.5%; Pred. No. 3.6e-20;
 Matches 48; Conservative 24; Mismatches 31; Indels 10; Gaps 5;

OY 1 QNMATFOCKHIKT-PIICNTILDNNTIYVGQCKRVNFTIISATYKACTGYI-NLN 58
 DB 24 QDWLTFCKHLLTRDVCNIMSTNLF---HCKDKNTFYISREPEYKALCKGIASKN 79
 OY 59 VLSSTRFOLNCTRTSITPR-PCPYSSRTETNYICVCKENCPVHPFAGIGRC 110
 DB 80 VLSNSEFYLAEC---NVAKPRCKYKLRKSSNRICRCEHLLPVHFGVGICP 129

RESULT 11

O9DFY8 PRELIMINARY: PRT: 128 AA.

ID O9DFY8:
 AC O9DFY8:
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RC-RNase2 ribonuclease precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OX NCB1_TaxID=8400;
 RN 11

SEQUENCE FROM N.A.

RC TISSUE=LIVER;
 RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
 RT "Purification and cloning of cytotoxic ribonucleases from Rana
 catesbeiana (bullfrog).";
 RL Nucleic Acids Res. 28:4097-4104(2000).
 RN 12

SEQUENCE FROM N.A.

RC TISSUE=LIVER;

